<110> Mahajan, Pramod B.

<120> Mre11 Orthologue and Uses Thereof

<130> 1264C

<150> US 09/835,654
<151> 2001-04-16

<150> US 60/198,570
<151> 2000-04-19

<160> 9

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<213> Zea mays

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acctgaactt aagctatttg gggctacttg tatttggaaa aaatatatcg ggtcctttac     120
tggtccgccg gtgttatttt aacttatgaa atg gtt ggt ttt tgc agt gca tta     174
                                    Met Val Gly Phe Cys Ser Ala Leu
                                     1               5

gat tta cag caa cgg att ggt ttg gcc aac acg ttg agt tca ggt tca      222
Asp Leu Gln Gln Arg Ile Gly Leu Ala Asn Thr Leu Ser Ser Gly Ser
     10              15                  20

atg tct gaa cca gca caa cct agt gga ggg gaa ggt gat gtc aac acg      270
Met Ser Glu Pro Ala Gln Pro Ser Gly Gly Glu Gly Asp Val Asn Thr
 25              30                  35                  40

ctc cga ata ctt gta gca acc gac tgc cat cta ggc tac atg gag aaa      318
Leu Arg Ile Leu Val Ala Thr Asp Cys His Leu Gly Tyr Met Glu Lys
                 45                  50                  55

gat gag ata cgt agg ttt gat tcc ttt caa gca ttt gag gag att tgc      366
Asp Glu Ile Arg Arg Phe Asp Ser Phe Gln Ala Phe Glu Glu Ile Cys
             60                  65                  70

gca ttg gca gat aaa aat aag gtg gat ttt ata ctt ctc ggt ggt gat      414
Ala Leu Ala Asp Lys Asn Lys Val Asp Phe Ile Leu Leu Gly Gly Asp
             75                  80                  85
```

```
cta ttc cat gag aac aag ccg tca cgc tca acc ctg gta aaa acg att          462
Leu Phe His Glu Asn Lys Pro Ser Arg Ser Thr Leu Val Lys Thr Ile
     90              95                  100

gag att cta cgg cgc tac tgc cta aat gat caa cct gtg aag ttc cag          510
Glu Ile Leu Arg Arg Tyr Cys Leu Asn Asp Gln Pro Val Lys Phe Gln
105                 110                 115                 120

gtt gtc agt gat cag aca gtt aac ttt cca aac agg ttt ggt aag gta          558
Val Val Ser Asp Gln Thr Val Asn Phe Pro Asn Arg Phe Gly Lys Val
                125                 130                 135

aat tat gaa gac cca aac ttt aac gtt ggt ctg cct gtg ttc acc att          606
Asn Tyr Glu Asp Pro Asn Phe Asn Val Gly Leu Pro Val Phe Thr Ile
                140                 145                 150

cat gga aat cat gat gac cct gct gga gtg gat aat ctc tct gct atc          654
His Gly Asn His Asp Asp Pro Ala Gly Val Asp Asn Leu Ser Ala Ile
            155                 160                 165

gat att ctt tcg gct tgc aat ctt gta aat tat ttt gga aag atg gac          702
Asp Ile Leu Ser Ala Cys Asn Leu Val Asn Tyr Phe Gly Lys Met Asp
    170                 175                 180

ctt ggt ggc tct ggc gtt ggt cag ata gca gtt tat cct gta ctt gta          750
Leu Gly Gly Ser Gly Val Gly Gln Ile Ala Val Tyr Pro Val Leu Val
185                 190                 195                 200

aaa aag ggc atg act tca gtt gca ctg tat ggt ctt gga aac att aga          798
Lys Lys Gly Met Thr Ser Val Ala Leu Tyr Gly Leu Gly Asn Ile Arg
                205                 210                 215

gat gaa cga cta aat aga atg ttt cag acg cct cat tca gta cag tgg          846
Asp Glu Arg Leu Asn Arg Met Phe Gln Thr Pro His Ser Val Gln Trp
            220                 225                 230

atg cga cct gga act caa gat ggg gag tca gcg tct gac tgg ttc aat          894
Met Arg Pro Gly Thr Gln Asp Gly Glu Ser Ala Ser Asp Trp Phe Asn
            235                 240                 245

ata ttg gta ctt cat cag aat agg ata aag aca aac cct aaa agt gcc          942
Ile Leu Val Leu His Gln Asn Arg Ile Lys Thr Asn Pro Lys Ser Ala
    250                 255                 260

atc aat gag cat ttc tta cca ggt tca tca gtc gcg acg tcc ctg att          990
Ile Asn Glu His Phe Leu Pro Gly Ser Ser Val Ala Thr Ser Leu Ile
265                 270                 275                 280

gat ggt gaa gca aaa cca aag cat gtt ctt ttg tta gaa atc aag gga          1038
Asp Gly Glu Ala Lys Pro Lys His Val Leu Leu Leu Glu Ile Lys Gly
                285                 290                 295

aat cag tac agg cca acc aaa ata cct ctg aga tct gtc aga cct ttt          1086
Asn Gln Tyr Arg Pro Thr Lys Ile Pro Leu Arg Ser Val Arg Pro Phe
                300                 305                 310
```

2

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gaa tat gct gag gtt gtg ttg aaa gat gaa gca gat gtt aac tca aat      1134
Glu Tyr Ala Glu Val Val Leu Lys Asp Glu Ala Asp Val Asn Ser Asn
        315             320             325

gat cag gac tct gtg ctt gaa cat ttg gat aaa att gta aga aat ctg      1182
Asp Gln Asp Ser Val Leu Glu His Leu Asp Lys Ile Val Arg Asn Leu
        330             335             340

att gag aag agt agc caa cca act gcc agc aga tca gag ccc aaa ctt      1230
Ile Glu Lys Ser Ser Gln Pro Thr Ala Ser Arg Ser Glu Pro Lys Leu
345             350             355             360

cca tta gtt aga atc aag gta gat tac tct ggg ttt tca aca ata aac      1278
Pro Leu Val Arg Ile Lys Val Asp Tyr Ser Gly Phe Ser Thr Ile Asn
                365             370             375


cca caa cgt ttt ggt cag aag tat gtt gga aag gtc gca aac cct caa      1326
Pro Gln Arg Phe Gly Gln Lys Tyr Val Gly Lys Val Ala Asn Pro Gln
                380             385             390

gat att ctc att ttc tca aaa tca gca aag aag cgc cag act aca gga      1374
Asp Ile Leu Ile Phe Ser Lys Ser Ala Lys Lys Arg Gln Thr Thr Gly
        395             400             405

gat cac att gat gat tct gag aaa ctt cgt cct gag gaa cta aac caa      1422
Asp His Ile Asp Asp Ser Glu Lys Leu Arg Pro Glu Glu Leu Asn Gln
        410             415             420

caa aca atc gaa gct ctg gtc gca gag agt aac ttg aaa atg gag att      1470
Gln Thr Ile Glu Ala Leu Val Ala Glu Ser Asn Leu Lys Met Glu Ile
425             430             435             440

ctt ccg gtt gat gat ttg gac att gcg ttg cat gat ttt gtg aac aag      1518
Leu Pro Val Asp Asp Leu Asp Ile Ala Leu His Asp Phe Val Asn Lys
                445             450             455

gat gac aag atg gca ttt tat tca tgt ttg cag aga aac ctt gaa gaa      1566
Asp Asp Lys Met Ala Phe Tyr Ser Cys Leu Gln Arg Asn Leu Glu Glu
                460             465             470

acc agg aat aag ttg agt tct gaa gca gat aaa tcc aaa ttt gag gaa      1614
Thr Arg Asn Lys Leu Ser Ser Glu Ala Asp Lys Ser Lys Phe Glu Glu
                475             480             485

gaa gat ata ata gtc aaa gtt ggc gag tgc atg cag gaa cgc gtt aag      1662
Glu Asp Ile Ile Val Lys Val Gly Glu Cys Met Gln Glu Arg Val Lys
        490             495             500

gaa agg tct ctg cac tct aag gac ggc aca cgt ttg aca aca ggc tct      1710
Glu Arg Ser Leu His Ser Lys Asp Gly Thr Arg Leu Thr Thr Gly Ser
505             510             515             520

cac aac ttg gtg ttt aat tat ctg agc ctt aat atc ttt tct ttt tgt      1758
His Asn Leu Val Phe Asn Tyr Leu Ser Leu Asn Ile Phe Ser Phe Cys
```

3

```
att ttt cct ggg gct gga tac tgg aca gct agt aac tct tac aac ctt    1806
Ile Phe Pro Gly Ala Gly Tyr Trp Thr Ala Ser Asn Ser Tyr Asn Leu
        540                    545                    550
```

```
taactaggat actggaggta aatctttac agctcaaagc aaccagaact ccttcagtga    1866
tgatgaagac accagggaga tgcttcttgg tgcaagatca actgatgttg acgaaaatc    1926
atctggattt actagaccct ccaaagatac tgctgatgtt gctaaacgtg gtacttccaa    1986
aagaggcagg ggaagaggca ccagttcaat gaagcagacc actcttagtt tcagccagtc    2046
aaggtcagct accgttattc gtagtgagga tgtggcttcc tctgaggagg aagcagatgc    2106
aaatgaagtt gttgaaaatt cagaagagga gagtgcgcaa caagttggac gtaaaagagc    2166
agctcctagg ggtagaggta gaggtagagg cggaggttcc actgcaaaga ggggcgaaa    2226
aacagatatt gcttccatgc aaaatatgat gagcaaagat gatgatgatt cagaagatga    2286
accgccaaag aaaactcctc gggtcaccag gaactatggc gctgtcagga ggagatgacc    2346
ctttaaggag ttcttgctca tgagagttat aggctaggtg ttttgtcttg taaagttgga    2406
agagccgacg tgttttatc aaccttgacg tcgaccagtt tgcgttgccg tgaactgact    2466
gtaccttgta cacgcccgaa tgtaacggat ttttgggatt tatacatcct tgtagctgct    2526
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aaaaaaaaaa a                                                        2597
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<211> 552
<212> PRT
<213> Zea mays

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Ala Asn Thr Leu Ser Ser Gly Ser Met Ser Glu Pro Ala Gln Pro Ser
            20                  25                  30
Gly Gly Glu Gly Asp Val Asn Thr Leu Arg Ile Leu Val Ala Thr Asp
        35                  40                  45
Cys His Leu Gly Tyr Met Glu Lys Asp Glu Ile Arg Arg Phe Asp Ser
    50                  55                  60
Phe Gln Ala Phe Glu Glu Ile Cys Ala Leu Ala Asp Lys Asn Lys Val
65                  70                  75                  80
Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser
                85                  90                  95
Arg Ser Thr Leu Val Lys Thr Ile Glu Ile Leu Arg Arg Tyr Cys Leu
            100                 105                 110
Asn Asp Gln Pro Val Lys Phe Gln Val Val Ser Asp Gln Thr Val Asn
        115                 120                 125
Phe Pro Asn Arg Phe Gly Lys Val Asn Tyr Glu Asp Pro Asn Phe Asn
    130                 135                 140
Val Gly Leu Pro Val Phe Thr Ile His Gly Asn His Asp Asp Pro Ala
145                 150                 155                 160
Gly Val Asp Asn Leu Ser Ala Ile Asp Ile Leu Ser Ala Cys Asn Leu
                165                 170                 175
Val Asn Tyr Phe Gly Lys Met Asp Leu Gly Gly Ser Gly Val Gly Gln
            180                 185                 190
Ile Ala Val Tyr Pro Val Leu Val Lys Lys Gly Met Thr Ser Val Ala
        195                 200                 205
Leu Tyr Gly Leu Gly Asn Ile Arg Asp Glu Arg Leu Asn Arg Met Phe
    210                 215                 220
Gln Thr Pro His Ser Val Gln Trp Met Arg Pro Gly Thr Gln Asp Gly
```

```
225                     230                     235                     240
Glu Ser Ala Ser Asp Trp Phe Asn Ile Leu Val Leu His Gln Asn Arg
                245                     250                     255
Ile Lys Thr Asn Pro Lys Ser Ala Ile Asn Glu His Phe Leu Pro Gly
                260                     265                     270
Ser Ser Val Ala Thr Ser Leu Ile Asp Gly Glu Ala Lys Pro Lys His
                275                     280                     285
Val Leu Leu Leu Glu Ile Lys Gly Asn Gln Tyr Arg Pro Thr Lys Ile
    290                     295                     300
Pro Leu Arg Ser Val Arg Pro Phe Glu Tyr Ala Glu Val Val Leu Lys
305                     310                     315                     320
Asp Glu Ala Asp Val Asn Ser Asn Asp Gln Asp Ser Val Leu Glu His
                325                     330                     335
Leu Asp Lys Ile Val Arg Asn Leu Ile Glu Lys Ser Ser Gln Pro Thr
                340                     345                     350
Ala Ser Arg Ser Glu Pro Lys Leu Pro Leu Val Arg Ile Lys Val Asp
                355                     360                     365
Tyr Ser Gly Phe Ser Thr Ile Asn Pro Gln Arg Phe Gly Gln Lys Tyr
    370                     375                     380
Val Gly Lys Val Ala Asn Pro Gln Asp Ile Leu Ile Phe Ser Lys Ser
385                     390                     395                     400
Ala Lys Lys Arg Gln Thr Thr Gly Asp His Ile Asp Asp Ser Glu Lys
                405                     410                     415
Leu Arg Pro Glu Glu Leu Asn Gln Gln Thr Ile Glu Ala Leu Val Ala
                420                     425                     430
Glu Ser Asn Leu Lys Met Glu Ile Leu Pro Val Asp Asp Leu Asp Ile
                435                     440                     445
Ala Leu His Asp Phe Val Asn Lys Asp Asp Lys Met Ala Phe Tyr Ser
    450                     455                     460
Cys Leu Gln Arg Asn Leu Glu Glu Thr Arg Asn Lys Leu Ser Ser Glu
465                     470                     475                     480
Ala Asp Lys Ser Lys Phe Glu Glu Glu Asp Ile Ile Val Lys Val Gly
                485                     490                     495
Glu Cys Met Gln Glu Arg Val Lys Glu Arg Ser Leu His Ser Lys Asp
                500                     505                     510
Gly Thr Arg Leu Thr Thr Gly Ser His Asn Leu Val Phe Asn Tyr Leu
                515                     520                     525
Ser Leu Asn Ile Phe Ser Phe Cys Ile Phe Pro Gly Ala Gly Tyr Trp
    530                     535                     540
Thr Ala Ser Asn Ser Tyr Asn Leu
545                     550
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<212> DNA
<213> Zea mays

<400> 4
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gtgatctatt ccatgagaac aagccgtcac gctcaaccct ggtaaaaacg attgagattc       180
tacggcgcta ctgcctaaat gatcaacctg tgaagttcca ggttgtcagt gatcagacag       240
ttaactttcc aaacaggttt ggtaaggtaa attatgaaga cccaaacttt aacgttggtc       300
tgcctgtgtt caccattcat ggaaatcatg atgaccctgc tggagtggat aatctctctg       360
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gctctggcgt tggtcagata gcagtttatc ctgtacttgt aaaaaagggc atgacttcag       480
ttgcactgta tggtcttgga acattagag atgaacgact aaatagaatg tttcagacgc       540
ctcattcagt acagtggatg cgacctggaa ctcaagatgg ggagtcagcg tctgactggt       600
tcaatatatt ggtacttcat cagaatagga taaagacaaa ccctaaaagt gccatcaatg       660
agcatttctt accaggttca tcagtcgcga cgtccctgat tgatggtgaa gcaaaaccaa       720
agcatgttct tttgttagaa atcaagggaa atcagtacag gccaaccaaa atacctctga       780
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caggagatca cattgatgat tctgagaaac ttcgtcctga ggaactaaac caacaaacaa      1140
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agagaaacct tgaagaaacc aggaataagt tgagttctga agcagataaa tccaaatttg      1320
aggaagaaga tataatagtc aaagttggcg agtgcatgca ggaacgcgtt aaggaaaggt      1380
ctctgcactc taaggacggc acacgtttga caacaggctc tcacaacttg gtgtttaatt      1440
atctgagcct taatatcttt tcttttttgta ttttttcctgg ggctggatac tggacagcta      1500
gtaactctta caacctttaa ctaggatact ggaggtaaat cttttacagc tcaaagcaac      1560
cagaactcct tcagtgatga tgaagacacc agggagatgc ttcttggtgc aagatcaact      1620
gatgttggac gaaaatcatc tggatttact agaccctcca aagatactgc tgatgttgct      1680
aaacgtggta cttccaaaag aggcagggga agaggcacca gttcaatgaa gcagaccact      1740
cttagtttca gccagtcaag gtcagctacc gttattcgta gtgaggatgt ggcttcctct      1800
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gttggacgta aaagagcagc tcctaggggt agaggtagag gtagaggcgg aggttccact      1920
gcaaagaggg ggcgaaaaac agatattgct tccatgcaaa atatgatgag caaagatgat      1980
gatgattcag aagatgaacc gccaaagaaa actcctcggg tcaccaggaa ctatggcgct      2040
gtcaggagga gatgaccctt taaggagttc ttgctcatga gagttatagg ctaggtgttt      2100
tgtcttgtaa agttggaaga gccgacgtgt ttttatcaac cttgacgtcg accagtttgc      2160
gttgccgtga actgactgta ccttgtacac gcccgaatgt aacggatttt tgggatttat      2220
acatccttgt agctgcttaa attccagcga ttgctgtcaa atgaacttcg ggaaaaaaaa      2280
aaaaaaaaaa aaaaaaaaaa aaaaaaaa                                        2308
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<210> 5
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<212> DNA
<213> Zea mays

<400> 5
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tcgacccacg cgtccggccg gcccttctct tcccttgctg ctgtgcgaac ccgagcgccc        60
aaacctgaac ttaagctatt tggggctact tgtatttgga aaaaatatat cgggtccttt       120
actggtccgc cggtgttatt ttaacttatg aaatggttgg tttttgcagt gcattagatt       180
```

6

```
tacagcaacg gattggtttg gccaacacgt tgagttcagg ttcaatgtct gaaccagcac      240
aacctagtgg aggggaaggt gatgtcaaca cgctcctaat acttgtagca accgactgcc      300
atctaggcta catggagaaa gatgagatac gtaggtttga ttccttttcaa gcatttgagg     360
agatttgcgc attggcagat aaaaataagg tggatt                                396
```

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        <210> 6
        <211> 36
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        <213> Artificial Sequence

        <220>
        <223> M13R synthetic primer

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agcggataac aatttcacac aggaaacagc tatgac                                 36
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        <210> 7
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        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> R1 synthetic primer

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cttatttttta tctgccaatg                                                  20
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        <210> 8
        <211> 25
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> T7 synthetic primer

        <400> 8
taatacgact cactataggg cgaat                                             25
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        <213> Artificial Sequence

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        <223> R2 synthetic primer

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gcgtgacggc ttgttctcat                                                   20
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